DSP-12, 1656 Base Pairs

AAGCAGTGGTAACAACGCAGAGTACGCGGGCGAGGAGAATATCTTGCTGGGAGTGGACT TTTCCAGTAAGGAAAGTAAAAGCTGCACCATTGGG**ATG**GTTCTCCGACTGTGGAGCGAC CATATTTAAGCCTGTGTCTGTCCAGGCCATGTGGTCTGCCCTGCAGGTGCTTCACAAGG CCTGCGAAGTGGCCCGGAGGCACAACTACTTCCCCGGGGGTGTAGCTCTCATCTGGGCT ACCTACTATGAGAGCTGCATCAGCTCCGAGCAGAGCTGCATCAACGAGTGGAACGCCAT GCAGGACCTGGAGTCTACGCGGCCCGACTCCCCCGCGCTATTTGTGGACAAGCCCACTG AAGGGGAAAGGACCGAGCGCCTCATCAAAGCCAAGCTCCGAAGCATCATGATGAGCCAG GATCTAGAAAATGTGACTTCCAAAGAGATTCGTAATGAATTAGAGAAACAGATGAATTG TAACTTGAAGGAACTCAAGGAATTTATAGACAATGAGATGCTACTTATCTTGGGACAGA TGGACAAGCCCTCCCTTATCTTCGATCATCTTTATCTCGGCTCTGAATGGAATGCATCC AATCTGGAGGAACTGCAGGGCTCAGGGGTTGATTACATTTTAAATGTTACCAGAGAAAT CGATAATTTTTTCCTGGCTTATTTGCATATCATAACATCCGAGTCTACGATGAAGAGA CCACAGACCTCCTCGCCCACTGGAATGAAGCGTATCATTTTATAAACAAAGCGAAGAGG AACCATTCCAAGTGCCTGGTGCATTGCAAAATGGGCGTGAGTCGCTCGGCCTCCACAGT CATAGCCTATGCAATGAAGGAATTCGGCTGGCCTCTGGAAAAAGCATATAACTATGTAA AGCAGAAGCGCAGCATCACGCGCCCCAACGCGGGCTTTATGAGGCAGCTGTCTGAGTAT CAGCAGCCTCCAGCAGCCTGTGGATGACCCTGCAGGACCTGGCGACTTCTTGCCAGAGA CCCCAGATGGCACCCCGGAAAGCCAGCTGCCCTTCTTGGATGATGCCGCCCAGCCCGGC TTAGGGCCCCCCTCCCCTGCTGTTTCCGGCGACTCTCAGACCCCCTTCTGCCTTCCCC AGGAAGCTGCTCCACCTGCAGAGGTGCACAGGCCGGCCAGACAGCCCCAGCAAGGTTCC GGACTCTGTGAGAAGGATGTGAAGAAGAAACTAGAGTTTGGGAGTCCCAAAGGTCGGAG CGGCTCCTTGCTGCAGGTGGAGGAGGACGGAAAGGGAGGAGGAGCCTGGGAGCAGGAGGT GGGGGCAGCTTCCAACCCAGCTCGATCAAAACCTGCTCAACTCGGAGAACCTAAACAAC AACAGCAAGAGGAGCTGTCCCAACGGCATGGAGGTAGGCAGAGCCCGGCCTGCAGGGTG GCACACCCCATCCCTTCCATCCCACTCTAATTGGCCTACCTCAGCCTCTGTAGTAGGGA AGCTCCCATCTCCAGGGACCTGAGGGTTCTTTCACAGGGTGATTCTGCTGGTGGGTACG TAGTGCATACCTTATATAGCAAATTGAGAATCTGTTGGGAATAACACATATCTCTGCAC ACCATCTTCACCCCATGTACCTTATTCATACCCTGGGCAGGGCTTCCAACTCAATTTCT AΑ

DSP-12, 552 Amino Acids

MVLRLWSDTKIHLDGDGGFSVSTAGRMHIFKPVSVQAMWSALQVLHKACEVARRHNYFP GGVALIWATYYESCISSEQSCINEWNAMQDLESTRPDSPALFVDKPTEGERTERLIKAK LRSIMMSQDLENVTSKEIRNELEKQMNCNLKELKEFIDNEMLLILGQMDKPSLIFDHLY LGSEWNASNLEELQGSGVDYILNVTREIDNFFPGLFAYHNIRVYDEETTDLLAHWNEAY HFINKAKRNHSKCLVHCKMGVSRSASTVIAYAMKEFGWPLEKAYNYVKQKRSITRPNAG FMRQLSEYEGILDASKQRHNKLWRQQTDSSLQQPVDDPAGPGDFLPETPDGTPESQLPF LDDAAQPGLGPPLPCCFRRLSDPLLPSPEDEAGSLVHLEDPEREALLEEAAPPAEVHRP ARQPQQGSGLCEKDVKKKLEFGSPKGRSGSLLQVEETEREEGLGAGRWGQLPTQLDQNL LNSENLNNNSKRSCPNGMEVGRARPAGWHTPSLPSHSNWPTSASVVGTTGTRHHTQLIF FYCLLWAPSSHLQGPEGSFTG

DSP-13, 1527 Base Pairs

CCTGGGAAGAAGTTATCTATCTCTCGAGTGACATTCAAGATATACCGTACCCCTCGGTTCTGTA ${\tt AGTCCTCTAAGTTGGAGGCATTCCATTCTGAGCCGGCCCC} \textbf{ATG} \textbf{ACCCTGAGCACGTTGGCCCGC}$ AAGAGGAAGGCGCCCTCGCTTGCACCTGCAGCCTCGGTGGCCCCGACATGATTCCTTACTTCT CCGCCAACGCGGTCATCTCGCAGAACGCCATCAACCAGCTCATCAGCGAGAGCTTTCTAACTGT CAAAGGTGCTGCCCTTTTTCTACCACGGGGAAATGGCTCATCCACACCAAGAATCAGCCACAGA CGGAACAAGCATGCAGGCGATCTCCAACAGCATCTCCAAGCAATGTTCATTTTACTCCGCCCAG AAGACAACATCAGGCTGGCTGTAAGACTGGAAAGTACTTACCAGAATCGAACACGCTATATGGT AGTGGTTTCAACTAATGGTAGACAAGACACTGAAGAAAGCATCGTCCTAGGAATGGATTTCTCC TCTAATGACAGTAGCACTTGTACCATGGGCTTAGTTTTGCCTCTCTGGAGCGACACGCTAATTC ATTTGGATGGTGATGGTTCAGTGTATCGACGGATAACAGAGTTCACATATTCAAACCTGT ATCTGTGCAGGCAATGTGGTCTGCACTACAGAGCTTACACAAGGCTTGTGAAGTCGCCAGAGCG CATAACTACCCAGGCAGCCTATTTCTCACTTGGGTGAGTTATTATGAGAGCCATATCAACT CAGATCAATCCTCAGTCAATGAATGGAATGCAATGCAAGATGTACAGTCCCACCGGCCCGACTC TTAAGGGAGATCATGATGCAGAAGGATTTGGAGAATATTACATCCAAAGAGATAAGAACAGAGT TGGAAATGCAAATGGTGTGCAACTTGCGGGAATTCAAGGAATTTATAGACAATGAAATGATAGT GATCCTTGGTCAAATGGATAGCCCTACACAGATATTTGAGCATGTGTTCCTGGGCTCAGAATGG AATGCCTCCAACTTAGAGGACTTACAGAACCGAGGGGTACGGTATATCTTGAATGTCACTCGAG AGATAGATAACTTCTTCCCAGGAGTCTTTGAGTATCATAACATTCGGGTATATGATGAAGAGGC AACGGATCTCCTGGCGTACTGGAATGACACTTACAAATTCATCTCTAAAGCAAAGAAACATGGA TCTAAATGCCTTGTGCACTGCAAAATGGGGGTGAGTCGCTCAGCCTCCACCGTGATTGCCTATG CAATGAAGGAATATGGCTGGAATCTGGACCGAGCCTATGACTATGTGAAAGAAGAAGACGAACGGT AACCAAGCCCAACCCAAGCTTCATGAGACAACTGGAAGAGTATCAGGGGATCTTGCTGGCAAGC TTCCTAGGCTTGATTCATGGAGGGAGGGACAAGCCCTGGGGAGAAAAGCACAGAATTTGAGT CAGTAGATCTGGTTTCCATTCCTGGTTCACCCTCTTGCTGCAACCCTGAGAAGTTACTTCACAT TTCTCATCCTTACCTGACCCCATCTATAAAATGAAAATCAAGAGATCCATCTCACAGGGTTATT

DSP-13, 509 Amino Acids

MTLSTLARKRKAPLACTCSLGGPDMIPYFSANAVISQNAINQLISESFLTVKGAALFLPRGNGS STPRISHRRNKHAGDLQQHLQAMFILLRPEDNIRLAVRLESTYQNRTRYMVVVSTNGRQDTEES IVLGMDFSSNDSSTCTMGLVLPLWSDTLIHLDGDGGFSVSTDNRVHIFKPVSVQAMWSALQSLH KACEVARAHNYYPGSLFLTWVSYYESHINSDQSSVNEWNAMQDVQSHRPDSPALFTDIPTERER TERLIKTKLREIMMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFE HVFLGSEWNASNLEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDTYKFISKAKKHGSKCL**VHCKMGVSRS**ASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEE YQGILLASFLGLIHGGRDKPWGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK

A DSP13 Alternate Splice Variant, 723 Base Pairs

CTGCCCGGCTTCTAACAGGCCACTGACCGGTACTCACTGGGGACCCACGCTCTAAGTTGTTGAT CTCTAGAACCGATTTTGGAAAAGGATTTGCCTTATTGAAGAAGACAGGATCATTCTTCTT AGACCTACTGAACGTGAACGAACAGAAAGGCTAATTAAAACCAAATTAAGGGAGATC**ATG**ATGC AGAAGGATTTGGAGAATATTACATCCAAAGAGATAAGAACAGAGTTGGAAATGCAAATGGTGTG CAACTTGCGGGAATTCAAGGAATTTATAGACAATGAAATGATAGTGATCCTTGGTCAAATGGAT AGCCCTACACAGATATTTGAGCATGTGTTCCTGGGCTCAGAATGGAATGCCTCCAACTTAGAGG AGGAGTCTTTGAGTATCATAACATTCGGGTATATGATGAAGAGGCAACGGATCTCCTGGCGTAC TGGAATGACACTTACAAATTCATCTCTAAAGCAAAGAAACATGGATCTAAATGCCTTGTGCACT GCAAAATGGGGGTGAGTCGCTCAGCCTCCACCGTGATTGCCTATGCAATGAAGGAATATGGCTG GAATCTGGACCGAGCCTATGACTATGTGAAAGAAGACGAACGGTAACCAAGCCCAACCCAAGC TTCATGAGACAACTGGAAGAGTATCAGGGGATCTTGCTGGCAAGCTTCCTAGGCTTGATTCATG GAGGGAGGACAAGCCCTGGGGAGAAAAGCACAGAATTTGAGTCAGTAGATCTGGTTTCCAT TCCTGGTTCACCCTCTTGCTGCAACCCTGAGAAGTTACTTCACATTTCTCATCCTTACCTGACC CCATCTATAAAA**TGA**AAATCAAGAGATCCATCTCACAGGGTTATTGTGAATAAAAATGTGTTTG AATGTTTATAAAAAAAAAAAAAAAAAAAA

B DSP13 Alternate Splice Variant, 241 Amino Acids

MMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFEHVFLGSEWNASN LEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDTYKFISKAKKHGSKCL VHCKMGVSRSASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEEYQGILLASFLGL IHGGRDKPWGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK

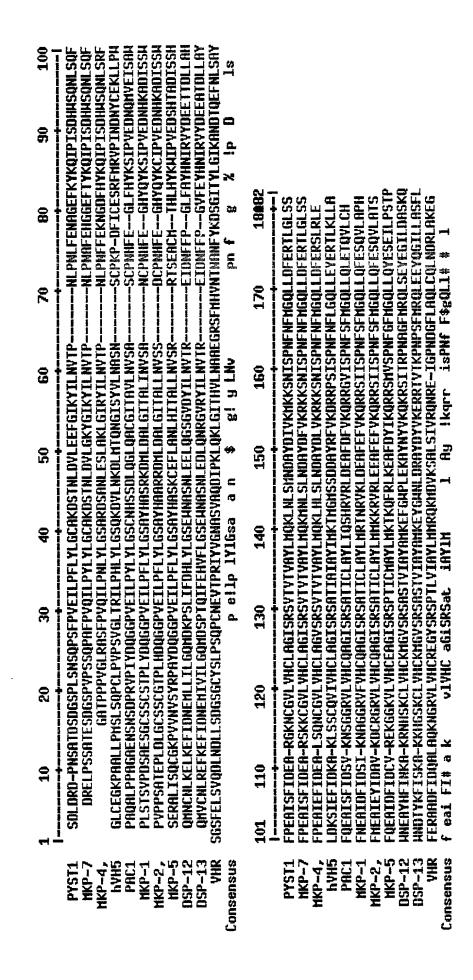


Figure 6

and DSP-13 **DSP-12** Alignment of



DSP-13 MTLSTLARKRKAPLACTCSLGGPDHIPYFSANAVISQNAINQLISESFLTVKGAALFLPRGNGSSTPRISHRRNKHAGDLQQHLQAAFILLRPEDNIRLAVRLESTYQNR

0 170 180 190 200 210 220	
10 150 1	TOTS
20 130 14	DSP-12 DSP-13 TRYMVVSTNGRQDTEESIVLGMDFSSNDS
111 120	DSP-12 DSP-13 TRYHVVS

330 LGSEHNR LGSEHNR
320 (PSLIFUHLY SPTQIFEHVF
310 HLILGOND! HIVILGOND!
300 KELKEFIDNE REFKEFIDNE
290 ELEKOMNCNL
280 ENVISKEIRNE ENITSKEIRTE
270 RSTHMSQOLE REIMMQKOLE
260 RTERLIKAKI RTERLIKAKI
250
240 i estrpospa ivoshrpospa
221 230 240 250 260 270 280 290 300 310 320 330 330 330 330 330 330 330 330 33
221 1 5SE09 NSD09
0SP-12 0SP-13

440 1 SITRPNN TVTKPNP
430 AYNYKOKR AYDYVKERR
420 HKEFGUPLEY HKEYGUNLDR
410 RSRSTVIRYR RSRSTVIRYR
400 LYHCKHGVSI
360 370 380 390 400 410 420 430 440 440 440 440 440 440 440 440 44
380 ANIMMERYIFT RYHNDI YKFT
370 .vydeettdli .vydeertdli
360 PGLERYINIR PGYFEYHNIR
331 340 350 360 360 SMLEELQGSGVDYII WYTREIDNFFPGLFA SNLEDLQMRGVRYILMYTREIDNFFPGVFE
340 ELQGSGVDYII DLQNRGVRYII
331 SNLE SNLE
0SP-12 0SP-13

550 EREALL
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530 DPLLPSPEDE
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500 GTPESQLPFL KLLHISHPYL
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480 Q-QPVDDPRG EFESVDLYSI
470 LURQQTDSSL RDKPHGEKST
441 450 460 470
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441 GFHR SFHR
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			DSP-12

